

SEQUENCE LISTING

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Darwish, Kamel El
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Li, Jin-Ping

<120> Glucuronyl C5-Epimerase, DNA Encoding the Same and Uses Thereof

<130> 1708.0280002

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<150> US 60/304,180

<151> 2000-12-08

<150> US 09/732,026

<151> 2000-12-08

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 1854

<212> DNA

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tgt gcg cta ttc act ttg gtc aca gta ctt ttg tgg aat aag tgt tcc	96
Cys Ala Leu Phe Thr Leu Val Thr Val Leu Leu Trp Asn Lys Cys Ser	
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agc gac aaa gca atc cag ttt cct cgg cac ttg agt agt gga ttc aga	144
Ser Asp Lys Ala Ile Gln Phe Pro Arg His Leu Ser Ser Gly Phe Arg	
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gtg gat gga tta gaa aaa aga tca gca gca tct gaa agt aac cac tat	192
Val Asp Gly Leu Glu Lys Arg Ser Ala Ala Ser Glu Ser Asn His Tyr	
50 55 60	
gcc aac cac ata gcc aaa cag cag tca gaa gag gca ttt cct cag gaa	240
Ala Asn His Ile Ala Lys Gln Gln Ser Glu Glu Ala Phe Pro Gln Glu	
65 70 75 80	
caa cag aag gca ccc cct gtt gtt ggg ggc ttc aat agc aac ggg gga	288
Gln Gln Lys Ala Pro Pro Val Val Gly Gly Phe Asn Ser Asn Gly Gly	
85 90 95	
agc aag gtg tta ggg ctc aaa tat gaa gag att gac tgt ctc ata aac	336
Ser Lys Val Leu Gly Leu Lys Tyr Glu Glu Ile Asp Cys Leu Ile Asn	
100 105 110	
gat gag cac acc att aaa ggg aga cga gag ggg aat gaa gtt ttc ctt	384
Asp Glu His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu	
115 120 125	
cca ttc act tgg gta gag aaa tac ttt gat gtt tat gga aaa gtg gtc	432
Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val	
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cag tat gac ggc tat gat cga ttt gaa ttc tct cat agc tat tcc aaa	480
Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys	
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Val Tyr Ala Gln Arg Ser Pro Tyr His Pro Asp Gly Val Phe Met Ser	
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Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser	
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Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr	
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Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys	
210 215 220	
aat cta acc gag aaa ccc cct cac ata gaa gta tat gaa aca gca gaa	720
Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr Ala Glu	
225 230 235 240	
gac agg gac aga aac atc aga cct aat gaa tgg act gtg ccc aag ggg	768

Asp Arg Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly	
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Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys	
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cag ttt att gct cca gaa acc agt gaa ggt gtg tct ttg cag ctg gga	864
Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly	
275 280 285	
aac aca aaa gac ttc att att tca ttt gac ctc aag ctt tta aca aat	912
Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Leu Leu Thr Asn	
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ggg agt gtg tct gtg gtt ctg gag acc aca gaa aag aat cag ctc ttc	960
Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe	
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act gtg cat tat gtc tca aac acc cag ctg att gct ttc aga gac agg	1008
Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Arg Asp Arg	
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gac ata tac tac ggc att ggg ccc aga act tca tgg agt aca gtt acc	1056
Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr	
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Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr	
355 360 365	
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Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu	
370 375 380	
att gca aaa ggg aag gga ttc ctg gac aac att acc atc tca acc aca	1200
Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr	
385 390 395 400	
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Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn	
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cag gat gag aaa ggt ggc tgg cca att atg gtg acc cgg aag tta ggg	1296
Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys Leu Gly	
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Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala Gln	
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Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys Asp	
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tat gta ttc ctc agt tca gct tta agg gca aca gcc cca tac aag ttt	1440
Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys Phe	
465 470 475 480	
ccg tca gag cag cat gga gtt aaa gcc gtg ttc atg aat aaa cat gac	1488
Pro Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys His Asp	
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Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly
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ttt atg tat tct tta att ggg ctg tat gac cta aaa gaa aca gca ggg 1584
Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly
515 520 525

gag aca ctt ggg aaa gaa gca agg tcc ttg tac gag cgc ggc atg gaa 1632
Glu Thr Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu
530 535 540

tct ctt aaa gcc atg ctg ccc ttg tat gat act ggc tcc ggg acc atc 1680
Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile
545 550 555 560

tat gac ctc cgc cac ttc atg ctt ggc att gct ccc aac ctg gcc cgc 1728
Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg
565 570 575

tgg gac tat cac acc acc cac att aac cag ctg cag ctg ctc agc acc 1776
Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr
580 585 590

atc gat gag tcc cca atc ttc aaa gaa ttt gtc aag agg tgg aaa agc 1824
Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser
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tac ctt aaa ggc agt agg gca aag cac aac 1854
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<212> PRT

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Ser Asp Lys Ala Ile Gln Phe Pro Arg His Leu Ser Ser Gly Phe Arg
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Val Asp Gly Leu Glu Lys Arg Ser Ala Ala Ser Glu Ser Asn His Tyr
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Ala Asn His Ile Ala Lys Gln Gln Ser Glu Glu Ala Phe Pro Gln Glu

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Pro	Phe	Thr	Trp	Val	Glu	Lys	Tyr	Phe	Asp	Val	Tyr	Gly	Lys	Val	Val
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Val	Tyr	Ala	Gln	Arg	Ser	Pro	Tyr	His	Pro	Asp	Gly	Val	Phe	Met	Ser
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Phe	Glu	Gly	Tyr	Asn	Val	Glu	Val	Arg	Asp	Arg	Val	Lys	Cys	Ile	Ser
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Phe	Tyr	Pro	Ile	Gln	Ile	Ala	Gln	Tyr	Gly	Leu	Ser	His	Tyr	Ser	Lys
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Asn	Leu	Thr	Glu	Lys	Pro	Pro	His	Ile	Glu	Val	Tyr	Glu	Thr	Ala	Glu
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Asp	Arg	Asp	Arg	Asn	Ile	Arg	Pro	Asn	Glu	Trp	Thr	Val	Pro	Lys	Gly
				245					250					255	
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			260					265					270		
Gln	Phe	Ile	Ala	Pro	Glu	Thr	Ser	Glu	Gly	Val	Ser	Leu	Gln	Leu	Gly
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	290					295					300				
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Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Arg Asp Arg
325 330 335

Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr
340 345 350

Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr
355 360 365

Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu
370 375 380

Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr
385 390 395 400

Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn
405 410 415

Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys Leu Gly
420 425 430

Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala Gln
435 440 445

Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys Asp
450 455 460

Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys Phe
465 470 475 480

Pro Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys His Asp
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Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly
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515 520 525

Glu Thr Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu
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Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile
545 550 555 560

Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg
565 570 575

Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr
580 585 590

Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser
595 600 605

Tyr Leu Lys Gly Ser Arg Ala Lys His Asn
610 615